I. AMENDMENT

IN THE SPECIFICATION:

Please delete paragraph [0024] and replace it with the following new paragraph:

[0024] The network 140 may provide access to the host server 130 that may be operated and maintained by an entity to provide information that may be downloaded to the terminal 120 and may relate to gene profiling data. It is foreseeable[[,]] that the user may access such a host server to download information, for example, gene profiling data in the database 1310 for use by the processor 1210. Moreover, it is foreseeable that the network interface 1240 may be used in conjunction with the bus 1220 and network 140 to upload information from the terminal 120 to the server 130 to augment information within the database 1310.

Please delete paragraph [0031] and replace it with the following new paragraph:

[0031] The expression profiling subsystem 110 may comprise, among other things, any high density, oligonucleotide probe micro-array, for example, an Affymetrix® GeneChip®. Such arrays provide efficient access to genetic information. Within such a probe array, a set of oligonucleotide probes to be synthesized is defined, based on its ability to hybridize to the target loci or genes of interest. The array generates, from control and treatment sets of cell-derived samples, respective sets of gene expression data representing a direction and a magnitude of regulation of each one of a high number of different nucleic acid sequences.

Please delete paragraph [0032] and replace it with the following new paragraph:

[0032] More specifically, by way of example, a sample of cells may be analyzed using an expression profiling array, such as an Affymetrix® GeneChip[[™]]® probe array for, for example, the human genome, which is capable of detecting over 65,000 sequences for that genome. Affymetrix[[™]]® provides a GeneChip[[™]]® fluidics station that automates the hybridization of nucleic acid targets to a probe array cartridge, and thus controls the delivery of reagents and the timing and temperature for hybridization. Each fluidics station can independently process four probe arrays at a given time.

Please delete paragraph [0032] and replace it with the following new paragraph:

[0033] Accordingly, each target may be prepared from a set of cell dishes or tissue samples by isolation of RNA over a course of time. ~~The treatment of those cells may be emulated by adding, for example, serum thereto.~~ Serum, for example, may be added to the cells to ensure a proper growth environment. At predetermined intervals, a small amount of the fluid is removed, and the cells are put in a quiescent state to stop the reaction time. Accordingly, a large set of targets, having a predetermined amount of liquid (e.g., .5 ml each) is produced. The GeneChip[[™]]® fluidics station may then hybridize each target, i.e., extract all the RNA and label the RNA by adding a chemical tag to each molecule, and control the delivery of the resulting liquid to the probe arrays to facilitate the obtaining of expression information regarding the mRNAs. The amount of mRNA is then ascertained based upon the signal strength of the reading given by the probe at the appropriate location corresponding to that sequence or sequence segment.

Please delete paragraph [0038] and replace it with the following new paragraph:

[0038] As shown in Figure 3, the Sample Preparation and Hybridization Phase 210 begins at 2105 and control proceeds to 2110. At 2110, the total RNA from a set of tissue samples is extracted, for example, RNAs of normal rat tissue samples: bladder, eye, heart, kidney, large intestine, small intestine, liver, pancreas, placenta, testis and skeletal muscle may be extracted using TRIZOL™ reagent (Life Technologies™ Inc., ~~Gaitherburg~~ Gaithersburg, MD). Control then proceeds to 2115, at which transcript integrity is monitored using, e.g., denaturing agorose gel electrophoresis.